

CORPORATE SOURCE: Natl. Inst. Neurol. Commun. Disorders Stroke,
 Natl. Inst. Health, Bethesda, MD, 20892, USA

SOURCE: EMBO Journal (1988), 7(7), 1947-55
 CODEN: EMJODG; ISSN: 0261-4189

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Genomic clones for the largest human neurofilament protein (NF-H) were isolated, the intron/exon boundaries mapped, and the entire protein-coding regions (exons) sequenced. The predicted protein contains a central region that obeys the structural criteria identified for α -helical 'rod' domains typically present in all intermediate filament (IF) protein components; it is .apprx.310 amino acids long, shares amino acid sequence homol. with other IF protein rod domains, and displays the characteristic heptad repeats of apolar amino acids which facilitate coiled-coil interaction. Nevertheless, anomalies are noted in the structure of the F-H rod which could explain observations of its poor homopolymeric assembly in vitro. The protein segment on the carboxy-terminal side of the human NF-H rod is uniquely long (>600 amino acids) compared to other IF proteins and is highly charged (>24% Glu, >25% Lys), rich in proline (>12%), and impoverished in cysteine, methionine, and aromatic amino acids. Its most remarkable feature is repetitive sequence that covers more than half its length and includes the sequence motif, Lys-Ser-Pro (KSP), >40 times. Together with the identification of the serine in KSP as the main target for NF-directed protein kinases *in vivo*, this repetitive character explains the massive phosphorylation of the NF-H subunit that can occur in axons. The human NF-H gene has three introns, two of which interrupt the protein-coding sequence at identical points to introns in the genes for the two smaller NF proteins, NF-M and NF-L. Both these introns differ from any of the several introns that have a common organization in all other (non-neural) IF genes. However, a clear evolutionary relationship between neural and non-neural IFs is now revealed by the observation that the third intron in the NF-H gene matches the position of one of the conserved introns in the non-neural IF gene pattern. Hence, divergence of the two IF lineages (neural from non-neural) is more likely to have involved ancestral IF gene duplication rather than RNA-mediated transposition.

IT 119213-37-5, Phosphoprotein NF-H (human clone HW10/HW12 subunit protein moiety reduced)

RL: PRP (Properties)

(amino acid sequence of)

E27 THROUGH E53 ASSIGNED

FILE 'REGISTRY' ENTERED AT 11:49:29 ON 26 MAY 2004

L3 27 SEA FILE=REGISTRY ABB=ON PLU=ON (391971-89-4/BI OR
 119213-37-5/BI OR 147388-28-1/BI OR 222963-40-8/BI OR
 329019-83-2/BI OR 329020-41-9/BI OR 329020-42-0/BI OR
 329020-43-1/BI OR 329020-44-2/BI OR 329020-45-3/BI OR
 329020-46-4/BI OR 329020-47-5/BI OR 329020-48-6/BI OR
 355029-63-9/BI OR 355043-60-6/BI OR 374653-90-4/BI OR
 400113-81-7/BI OR 400154-00-9/BI OR 409392-10-5/BI OR
 419604-01-6/BI OR 420909-41-7/BI OR 437023-11-5/BI OR
 528612-99-9/BI OR 538425-66-0/BI OR 538458-06-9/BI OR

611252-43-8/BI OR 612112-12-6/BI)

L4 27 L1 AND L3

L4 ANSWER 1 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 612112-12-6 REGISTRY
 CN Protein (human heart clone GenBank gi:10835089 mitochondria-associated) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 1115: PN: WO03087768 SEQID: 1115 claimed protein
 CI MAN
 SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSH
 51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
 101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
 151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
 201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
 251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
 301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
 351 DRHQADIASY QEAQQLDAE LRNTKWEAAA QLREYQDLLN VKMALDIEIA
 401 AYRKLLGEEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKS EEKIKVVEKS
 451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
 501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEEA KSPEKEEAKS PAEVKSPEKA
 551 KSPAKEEAKS PPEAKSPEKE EAKSPAEVKS PEAKSPAKE EAKSPAEEAKS
 601 PEAKSPVKE EAKSPAEEAKS PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
 651 KAKSPEAKS PEKEEAKSPE KAKSPVKAEE KSPEAKAKSPV KAEAKSPEKA
 =
 701 KSPVKEEAKS PEAKSPVKE EAKSPEAKS PVKEEAKTPE KAKSPVKEEA
 ===== = ===== = =====
 751 KSPEAKAKSPE KAKTLDVKSP EAKTPAKEEA RSPADKFPEK AKSPVKEEVK
 =====
 801 SPEAKAKSPLK EDAKAPEKEI PKKEEVKSPV KEEEKPKQEVK VKEPPKKAAEE
 851 EKAPATPKTE EKKDSKKEEA PKKEAKPKV EKKEAPEVEK PKESKVEAKK
 901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPK EKTEVAKKEPD DAKAKEPSKP
 951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTLSK EPSKPKAEKA
 1001 EKSSSTDQKD SKPPEKATED KAAKGK

HITS AT: 700-731, 742-759

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:333132

L4 ANSWER 2 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 611252-43-8 REGISTRY
 CN Protein (human clone US20030194704-SEQID-32114 exon-derived fragment) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 114: PN: US20030194704 SEQID: 32114 claimed protein
 CI MAN
 SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
 51 TVIVEEQTEE TQVTEEVTEE EEEKEAKEEEG KEEEGGEEEEE AEGGEEETKS
 101 PPAEEAASPE KEAKSPVKEE AKSPAEEAKSP EKKEAKSPAEE VKSPEAKSP
 151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEAK SPAEAKSPEK

201 AKSPVKEEAK SPAEKSPVK EEAKSPEVK SPEKAKSPTK EEAKSPEKAK
 251 SPEKEEAKSP EAKSPVKAE AKSPEKAKSP VKAEAKSPEK AKSPVKEEAK

301 SPEKAKSPVK EEAKSPEKAK SPVKEEAKTP EAKSPVKEE AKSPEKAKSP

351 EAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
 401 KADAKAPEKE IPKKEEVKSP VKEEKPQEV KVKEPPKAE EEKAPATPKT
 451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKV
 501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
 551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSPKPKAEK AEKSSSTDQK
 601 DSKPPEKATE DKAAGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:303033

L4 ANSWER 3 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 538458-06-9 REGISTRY
 CN Pain-regulated protein (human clone WO03016475-SEQID-9347) (9CI)
 (CA INDEX NAME)

OTHER NAMES:

CN 2255: PN: WO03016475 SEQID: 9347 claimed protein
 CI MAN
 SQL 1020

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHWS
 51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ

101 LQALNDRFAG YIDKVRQLEA HNRSLGEAA ALRQQQAGRS AMGELYEREV
 151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAAAR
 201 ALARFAQEAE AARVDLQKKA QALQEECGYL RRHHQEEVG ELLGQIQGSGA
 251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
 301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
 351 DRHQADIASY QEAIQQLDAE LRNTKWEAMA QLREYQDLLN VKMALDIEIA
 401 AYRKLLGEEE CRIGFGPIPF SLPEGLPKIP SVSTHIVKVS EEKIKVVEKS
 451 EKETVIVEEQ TEETQVTEEF TEEEKEAKE EEGKEEEGGE EEEAEGGEEE
 501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEE KSPEKEEAKS PAEVKSPEKA
 551 KSPAKEEAKS PPEAKSPEKE EAKSPAEVKS PPEAKSPA EAKSPAEEAKS
 601 PEAKSPVKE EAKSPAEEAKS PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
 651 KAKSPEKEA KSPEAKSPV KAEAKSPEKA KSPVKAEEAKS PEAKSPVKE

701 EAKSPEAKS PVKEEAKSPE KAKSPVKEEA KTPEKAKSPV KEEAKSPEKA

751 KSPEAKTLD VKSPEAKTPA KEEARSPADK FPEAKSPV EEVKSPEAK
 ===

801 SPLKADAKAP EKEIPKKEEV KSPVKEEKP QEVKVKEPPK KAEEEKAPAT
 851 PKTEEKDSK KEEAPKKEAP KPKVEEKKEP AVEKPKESKV EAKKEEAEDK
 901 KKVPTEPEKA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
 951 APEKKDTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKAEKSSST
 1001 DQKDSKPEK ATEDKAAGK

HITS AT: 694-725, 736-753

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:18399

09/847586

L4 ANSWER 4 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 538425-66-0 REGISTRY
CN Pain-regulated protein (human clone WO03016475-SEQID-4798) (9CI)
(CA INDEX NAME)
OTHER NAMES:
CN 2214: PN: WO03016475 SEQID: 4798 claimed protein
CI MAN
SQL 1020

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDSLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTSA LREIRAOLEG HAVOSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAQQLDAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
401 AYRKLLGEET CRIGFGPIPF SLPEGLPKIP SVSTHIKVKS EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEA KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPAEVKS PEAKSPAKE EAKSPAEAKS
601 PEAKSPVKE EAKSPAEAKS PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
651 KAKSPEKEEA KSPEAKSPV KAEAKSPEKA KSPVKAEEAKS PEAKSPVKE
=====
701 EAKSPEAKS PVKEEAKSPE KAKSPVKEEA KTPEAKSPV KEEAKSPEKA
=====
751 KSPEAKTLD VKSPEAKTPA KEEARSPADK FPEAKSPVKE EEVKSPEAK
====
801 SPLKADAKAP EKEIPKKEEV KSPVKEEEKP QEVKVKEPPK KAEKKAPAT
851 PKTEEKKDSK KEEAKPKKEAP KPKVEEKKEP AVEKPKESKV EAKKEEAEDK
901 KKVPTPEKEA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
951 APEKKDTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKAEKSSST
1001 DQKDSKPPEK ATEDKAAGKG

HITS AT: 694-725, 736-753

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 139:18398

L4 ANSWER 5 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 528612-99-9 REGISTRY
CN Protein (human gene CG4399 sequence homolog) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 130: PN: WO03040301 PAGE: 197-198 claimed protein
CN Putative neurofilament protein (human)
CI MAN
SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDSLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTSA LREIRAOLEG HAVOSTLQSE EWFRVRLDRL
301 SEAAKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAQQLDAE IRNTKWEMAA QLREYQDLLN VKMALDIEIA

Searcher : Shears 571-272-2528

09/847586

401 AYRKLLLEGEE CRIGFGPIPF SLPEGLPKIP SVSTHIKVKS EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPAEC KSPEKEEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPAEVKS PEAKSPAEC EAKSPAEC
601 PEAKSPVKE EAKSPAEC KSPEAKSPV PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
651 KAKSPEAKS PEKEEAKSPE KAKSPVKAEC KSPEAKSPV KAEAKSPEKA
=

701 KSPVKEEAKS PEAKSPVKE EAKSPAEC KSPEAKSPV PVKEEAKTPE KAKSPVKEEA
===== ===== ===== = =====
751 KSPEAKSPE KAKTLDVKSP EAKTPAEEA RSPADKFPEK AKSPVKEEVK
=====

801 SPEKAKSPLK EDAKAPEKEI PKKEEVKSPV KEEEKPKQEVK VKEPPKKAEE
851 EKAPATPKTE EKDKSKKEEA PKKEAPKPKV EEKKEPAVEK PKESKVEAKK
901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPK KTEVAKKEPD DAKAKEPSKP
951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTLSK EPSKPKAeka
1001 EKSSSTDQKD SKPPEKATED KAAKGK

HITS AT: 700-731, 742-759

REFERENCE 1: 138:397302

L4 ANSWER 6 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 437023-11-5 REGISTRY
CN Protein (human clone US20020048763-SEQID-36182 exon-encoded
fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 1177: PN: US20020048763 SEQID: 36182 claimed protein

CI MAN

SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEEKEAKEEG KEEEGGEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPAEC KEEAKSPAEC VKSPEAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEC EAKSPAEC
201 AKSPVKEEAK SPAEKSPVKE EAKSPAECV SPEAKSPTK EAKSPAEC
251 SPEKEEAKSP EKAKSPVKAEC AKSPEAKSP VKEEAKSPEK AKSPVKEEAK
=====

301 SPEKAKSPVKE EAKSPAEC SPVKEEAKTP EKAKSPVKEE AKSPEAKSP
===== ===== = =====
351 EKAKTLDVKS PEAKTPAEEA RSPADKFPE KAKSPVKEEV KSPEAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEKPQEVV KVEPPKKAEE EKAPATPKT
451 EKDKSKKEEA PKKEAPKPK VEEKKEPAVE KPKESKVEAK KEEAEDKKKVP
501 TPEKEAPAK VEVKEDAKPK KTEVAKKEPD DAKAKEPSKP PAEKKEAAPE
551 KDTKEEKAKK PEEKPKTEAK KAKEDDKTLSK KEPSPKKAEC AEKSSSTDQKD
601 DSKPPEKATE DKAKGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:28982

L4 ANSWER 7 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 420909-41-7 REGISTRY
CN Protein (human clone WO01057273-SEQID-28953 exon-encoded fragment)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2760: PN: WO01057273 SEQID: 28953 claimed protein

Searcher : Shears 571-272-2528

CI MAN
SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSVP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
 51 TVIVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEEE AEGGEEETKS
 101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA VKSPEAKSP
 151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
 201 AKSPVKEEAK SPAEAKSPV EEAKSPEEVK SPEAKSPTK EEAKSPEAK
 251 SPEKEEAKSP EKAkSPVKAk AKSPEAKSP VKAkEAKSPEK AKSPVKEEAK
 =====
 301 SPEAKSPV EEAkSPEAK SPVKEEAKTP EKAkSPVKEE AKSPEAKSP
 =====
 351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
 401 KADAKAPEKE IPKKEEVKSP VKEEKPQEV KVKEPPKAE EEKAPATPKT
 451 EEEKKDSKKEE APkKEAPKPK VEEKKEPAVE KPKEskVKEAK KEEAEDKKKV
 501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
 551 KKDTKEEAK KPEEKPKTEA KAKEDDKTLS KEPSPKKAk AEKSSSTDQK
 601 DSKPPEKATE DKAkGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351355

L4 ANSWER 8 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 419604-01-6 REGISTRY
 CN Protein (human cervix cell clone WO0157278-SEQID-21284 exon-encoded
 fragment) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 1884: PN: WO0157278 SEQID: 21284 claimed protein
 CI MAN
 SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSVP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
 51 TVIVEEQTEE TQVTEEVTEE EEKEAKEEEG KEEEGGEEEEE AEGGEEETKS
 101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA VKSPEAKSP
 151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
 201 AKSPVKEEAK SPAEAKSPV EEAKSPEEVK SPEAKSPTK EEAKSPEAK
 251 SPEKEEAKSP EKAkSPVKAk AKSPEAKSP VKAkEAKSPEK AKSPVKEEAK
 =====
 301 SPEAKSPV EEAkSPEAK SPVKEEAKTP EKAkSPVKEE AKSPEAKSP
 =====
 351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
 401 KADAKAPEKE IPKKEEVKSP VKEEKPQEV KVKEPPKAE EEKAPATPKT
 451 EEEKKDSKKEE APkKEAPKPK VEEKKEPAVE KPKEskVKEAK KEEAEDKKKV
 501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
 551 KKDTKEEAK KPEEKPKTEA KAKEDDKTLS KEPSPKKAk AEKSSSTDQK
 601 DSKPPEKATE DKAkGK

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351347

L4 ANSWER 9 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 409392-10-5 REGISTRY

09/847586

CN Protein (human brain clone WO0157275-SEQID-28374 exon-encoded fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2394: PN: WO0157275 SEQID: 28374 claimed protein

CI MAN

SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA VKSPEAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
201 AKSPVKEEAK SPAEAKSPVK EEAKSPEAKV SPEAKSPTK EEAKSPEAK
251 SPEKEEAKSP EKAKSPVKA AKSPEAKSP VKAEEAKSPEK AKSPVKEEAK
=====

301 SPEAKSPVK EEAKSPEAK SPVKEEAKTP EKAKSPVKEE AKSPEAKSP
=====

351 EKAKTLDVKS PEAKTPAKKE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKKAEE EEKAPATPKT
451 EKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSPKPKAE AEKSSSTDQK
601 DSKPPEKATE DKAAGKG

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:305084

L4 ANSWER 10 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN

RN 400154-00-9 REGISTRY

CN Protein (human fetal liver clone WO0157277-SEQID-28080 exon-encoded fragment) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2295: PN: WO0157277 SEQID: 28080 claimed protein

CI MAN

SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
51 TVIVEEQTEE TQVTEEVTEE EEEKEAKEEEG KEEEGGEEEE AEGGEEETKS
101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA VKSPEAKSP
151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
201 AKSPVKEEAK SPAEAKSPVK EEAKSPEAKV SPEAKSPTK EEAKSPEAK
251 SPEKEEAKSP EKAKSPVKA AKSPEAKSP VKAEEAKSPEK AKSPVKEEAK
=====

301 SPEAKSPVK EEAKSPEAK SPVKEEAKTP EKAKSPVKEE AKSPEAKSP
=====

351 EKAKTLDVKS PEAKTPAKKE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKKAEE EEKAPATPKT
451 EKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSPKPKAE AEKSSSTDQK
601 DSKPPEKATE DKAAGKG

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

Searcher :

Shears

571-272-2528

REFERENCE 1: 136:178933

L4 ANSWER 11 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 400113-81-7 REGISTRY
 CN Protein (human clone WO0157274-SEQID-22654 exon-encoded fragment)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 2061: PN: WO0157274 SEQID: 22654 claimed protein
 CI MAN
 SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
 51 TVIVEEQTEE TQVTEEVTEE EEEKEAKEEEK KEEEGGEEEEE AEGGEEETKS
 101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA VKSPEAKSP
 151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
 201 AKSPVKEEAK SPAEKSPVK EEAKSPEEVK SPEAKSPTK EEAKSPEAK
 251 SPEKEEAKSP EKAKSPVKA AKSPEAKSP VKAEAKSPEK AKSPVKEEAK
 ======
 301 SPEAKSPVK EEAKSPEAK SPVKEEAKTP EKAKSPVKEE AKSPEAKSP
 ======
 351 EKAKTLDVKS PEAKTPAKKE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
 401 KADAKAPEKE IPKKEEVKSP VKEEEKPQEV KVKEPPKAE EEKAPATPKT
 451 EEKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKKV
 501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
 551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSPKPKAEK AEKSSSTDQK
 601 DSKPPEKATE DKAAGKG

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:195264

L4 ANSWER 12 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 391971-89-4 REGISTRY
 CN Heavy neurofilament subunit (human gene NF-H) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 4211: PN: WO03038130 FIGURE: 3 claimed protein
 CN GenBank CAA33366
 CN GenBank CAA33366 (Translated from: GenBank X15306)
 CI MAN
 SQL 1020

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSW
 51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
 101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
 151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQLLDEAR QREEAAEAAAR
 201 ALARFAQEAE AARVDLQKKA QALQECEGYL RRHHQEEVGE LLGQIQGSGA
 251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
 301 SEAAKVNTDA MRSAQEEITE YRRLQQARTT ELEALKSTKD SLERQRSELE
 351 DRHQADIASY QEAIQQLDAE LRNTKWEMAA QLREYQDLLN VKMALDIEIA
 401 AYRKLEGE CRIGFGPIPF SLPEGLPKIP SVSTHIVKS EEKIVVVEKS
 451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEGKEEEGGE EEEAEGGEEEEE
 501 TKSPPAEEAA SPEKEAKSPV KEEAKSPA EKSPKEEAKS PAEVKSPEKA
 551 KSPAEEKS PPEAKSPEKE EAKSPAEVKS PEAKSPA EAKSPA EAKSPA
 601 PEAKSPVKE EAKSPA EAKSPVKE PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
 651 KAKSPEKEEA KSPKEAKSPV KAEAKSPEKA KSPVKA EAKSPEKA PEAKSPVKE

=====

701 EAKSPEAKS PVKEEAKSPE KAKSPVKEEA KTPEKAKSPV KEEAKSPEKA
 =====

751 KSPEAKTLD VKSPEAKTPA KEEARSPADK FPEKAKSPVK EEVKSPEKAK
 ===

801 SPLKADAKAP EKEIPKKEEV KSPVKEEEKP QEVKVKEPPK KAEEEKAPAT
 851 PKTEEKKDSK KEEAPKKEAP KPKVEEKKEP AVEKPESKV EAKKEEAEDK
 901 KKVPTPEKEA PAKVEVKEDA KPKEKTEVAK KEPDDAKAKE PSKPAEKKEA
 951 APEKKDTKEE KAKKPEEKPK TEAKAKEDDK TLSKEPSKPK AEKAEKSSST
 1001 DQKDSKPPEK ATEDKAAKGK

HITS AT: 694-725, 736-753

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:380506

REFERENCE 2: 136:146104

L4 ANSWER 13 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 374653-90-4 REGISTRY
 CN Protein (human HBL100 cell clone WO0157270-SEQID-12927 exon-encoded
 fragment) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 2869: PN: WO0157270 SEQID: 12927 claimed protein
 CI MAN
 SQL 617

SEQ 1 KLLEGEECRI GFGPIPFSLP EGLPKIPSVS THIKVKSEEK IKVVEKSEKE
 51 TVVVEEQTEE TQVTEEVTEE EKEAKEEEG KEEEGGEEE AEGGEEETKS
 101 PPAEEAASPE KEAKSPVKEE AKSPAEEKSP EKEEAKSPA EVKSPVKEE
 151 AKEEAKSPPE AKSPEKEEAK SPAEVKSPEK AKSPAEEK SPAEAKSPEK
 201 AKSPVKEEAK SPAEAKSPVK EEAKSPEAK SPAEAKSPVK EEAKSPEAK
 251 SPEKEEAKSP EKAKSPVKEA AKSPEAKSP VKEAKSPEK AKSPVKEEAK
 =====

301 SPEAKSPVK EEAKSPEAK SPVKEEAKTP EKAKSPVKEE AKSPEAKSP
 =====

351 EKAKTLDVKS PEAKTPAKEE ARSPADKFPE KAKSPVKEEV KSPEAKSPL
 401 KADAKAPEKE IPKKEEVKSP VKEEKPQEV KVKEPPKAE EEKAPATPKT
 451 EKKDSKKEE APKKEAPKPK VEEKKEPAVE KPESKVEAK KEEAEDKKV
 501 PTPEKEAPAK VEVKEDAKPK EKTEVAKKEP DDAKAKEPSK PAEKKEAAPE
 551 KKDTKEEKAK KPEEKPKTEA KAKEDDKTLS KEPSPKPKAE AEKSSTDQK
 601 DSKPPEKATE DKAAGKG

HITS AT: 291-322, 333-350

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:1595

L4 ANSWER 14 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 355043-60-6 REGISTRY
 CN Protein (human clone 787CIP2B_152 contig-encoded fragment) (9CI)
 (CA INDEX NAME)
 OTHER NAMES:
 CN 338: PN: WO0157190 SEQID: 3455 claimed sequence
 CI MAN
 SQL 1033

SEQ 1 APTAQAMMSF GGADALLGAP FAPLHGGSSL HYALARKGGA GGTRSAAGSS
 51 SGFHSWTRTS VSSVSASPSR FRGAGAASST DSILDTLSNGP EGCMVAVATS
 101 RSEKEQLQAL NDRFAGYIDK VRQLEAHNRS LEGEAAALRQ QQAGRSAMGE
 151 LYEREVREMR GAVLRLGAAR GQLRLEQEH LEDIAHVRQR LDDEARQREE
 201 AEAAAALAR FAQEAEAAARV DLQKKAQALQ EECGYLRRHH QEEVGELLGQ
 251 IQGSGAAQAAQ MQAETRDALK CDVTSALREI RAQLEGHAVQ STLQSEEWFR
 301 VRLDRLSEAA KVNTDAMRSA QEEITEYRRQ LQARTTELEA LKSTKDSLTER
 351 QRSELEDRHQ ADIASYQEAI QQLDAELRNT KWEMAAQLRE YQDLLNVKMA
 401 LDIEIAAYRK LLEGEECRIG FGPIPFSLPE GLPKIPSST HIKVKSEEKI
 451 KVVEKSEKET VIVEEQTEET QVTEEVTEEE DKEAKEEEKG EEEGEEEEA
 501 EGGEETKSP PAEEAASPEK EAKSPVKEEA KSPAEAKSPE KEEAKSPAEV
 551 KSPEKAKSPA KEEAKSPPEA KSPEKDGKQN FQAEVKSPEK AKSPAEEAK
 601 SPAEAKSPEK AKSPVKEEAK SPAEAKSPVK EEAKSPEAK SPEAKSPTK
 651 EEAKSPEKAK SPEAKSPEK EEAKSPEKAK SPVKAEEAKSP EAKSPVKA
 701 AKSPEKAKSP VKEEAKSPEK AKSPVKEEAK SPEAKSPEK EEAKSPEKAK
 =====
 751 SPVKEEAKSP EAKSPEKAK TLDVKSPEAK TPAKEEARSP ADKFPEAKS
 =====
 801 PVKEEVKSPE KAKSPLKEDA KAPEKEIPKK EEVKSPVKEE EKPQEVKVKE
 851 PPKKAAEEKA PATPKTEEKK DSKKEEAPKK EAPPKVVEEK KEPAVEKPKE
 901 SKVEAKKEA EDKKKVPTPE KEAPAKVEVK EDAKPKEKTE VAKKEPDDAK
 951 AKEPSKPAEK KEEAPEKKDT KEEKAKKPEE KPKTEAKAKE DDKTLKSKEPS
 1001 KPKAEEKA KSSTDQKDSKP PEKATEDKAA KGK

HITS AT: 707-738, 749-766

REFERENCE 1: 135:176460

L4 ANSWER 15 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
 RN 355029-63-9 REGISTRY
 CN Protein (human clone 787CIP2B_152) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN 795: PN: WO0157190 SEQID: 1487 claimed protein
 CI MAN
 SQL 1026

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSW
 51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
 101 LQALNDRFAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
 151 REMRGAVLRL GAARGQLRL QEHLLEDIAH VRQLLDDEAR QREEAEAAAR
 201 ALARFAQEAE AARVDLQKKA QALQECEGYL RRHHQEEVGE LLGQIQGSGA
 251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
 301 SEAALKVNTDA MRSAQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
 351 DRHQADIASY QEAQQLDAE LRNTKWEAA QLREYQDILLN VKMALDIEIA
 401 AYRKLEGE CRIGFGPIPF SLPEGLPKIP SVSTHIVKS EEKIVVVEKS
 451 EKETVIVEEQ TEETQVTEEV TEEEEEKEAKE EEEGKEEKG EEEAEGGEEE
 501 TKSPPVVEAA SPEKEAKSPV KEEAKSPA EA KSPKEEAKS PAEVKSPEKA
 551 KSPKEEAKS PPEAKSPEKE EAKSPAEVKS PEKAKSPA EAKSPA EAKSPEAKS
 601 PEAKSPVKE EAKSPA EAKSPEAKS PVKEEAKSPA EVKSPEAKS PTKEEAKSPE
 651 KAKSPEAKS PEKEEAKSPE KAKSPVKEA KSPKEAKSPV KAEAKSPEKA
 =
 701 KSPVKEEAKS PEAKSPVKE EAKSPEAKS PVKEEAKTPE KAKSPVKEEA
 =====
 751 KSPKEAKSPE KAKTLDVKSPE EAKTPAKEEA RSPADKFPEK AKSPVKEEVK
 =====
 801 SPEAKSPLK EDAKAPEKEI PKKEEVKSPV KEEEPQEVK VKEPPKKAEE

09/847586

851 EKAPATPKTE EKKDSKKEEA PKKEAPKPKV EEKKEPAVEK PKESKVEAKK
901 EEAEDKKKVP TPEKEAPAKV EVKEDAKPKE KTEVAKKEPD DAKAKEPSKP
951 AEKKEAAPEK KDTKEEKAKK PEEKPKTEAK AKEDDKTLSK EPSPKKAEKA
1001 EKSSSTDQKD SKPPEKATED KAAKGK
HITS AT: 700-731, 742-759

REFERENCE 1: 135:176460

L4 ANSWER 16 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-48-6 REGISTRY
CN L-Valinamide, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl- (9CI) (CA INDEX NAME)
SQL 19

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

REFERENCE 1: 134:204745

L4 ANSWER 17 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-47-5 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 18 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-46-4 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 19 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-45-3 REGISTRY

Searcher : Shears 571-272-2528

09/847586

CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 20 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-44-2 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 21 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-43-1 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-O-phosphono-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 22 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 329020-42-0 REGISTRY
CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEKAKSP
=====

Searcher : Shears 571-272-2528

09/847586

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 23 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN **329020-41-9** REGISTRY
CN L-Proline, L-alanyl-L-lysyl-O-phosphono-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI)
(CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 24 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN **329019-83-2** REGISTRY
CN L-Proline, L-alanyl-L-lysyl-L-seryl-L-prolyl-L-valyl-L-lysyl-L- α -glutamyl-L- α -glutamyl-L-alanyl-L-lysyl-L-seryl-L-prolyl-L- α -glutamyl-L-lysyl-L-alanyl-L-lysyl-L-seryl- (9CI)
(CA INDEX NAME)
SQL 18

SEQ 1 AKSPVKEEAK SPEAKSP
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:204745

L4 ANSWER 25 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN **222963-40-8** REGISTRY
CN Protein (human brain gene KIAA0845 C-terminal fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAA74868
CN GenBank BAA74868 (Translated from: GenBank AB020652)
CI MAN
SQL 1034

SEQ 1 NPISTAQAMM SFGGADALLG APFAPLHGGG SLHYALARKG GAGGTRSAAG
51 SSSGFHSWTR TSVSSVSASP SRFRGAGAAS STDSLDTLSN GPEGCMVAVA
101 TSRSEKEQLQ ALNDRFAGYI DVKVRQLEAHN RSLEGEAAAL RQQQAGRSAM
151 GELYEREVRE MRGAVLRLGA ARGQLRLEQE HLLEDIAHVR QRLDDEARQR
201 EEAEEAARAL ARFAQEAEAA RVDLQKKAQA LQEECGYLRR HHQEEVGELL
251 GQIQGSGAAQ AQMQAETRDA LKCDVTSALR EIRAQLEGHA VQSTLOSEEW
301 FRVRLDRLSE AAKVNTDAMR SAQEEITEYR RQLQARTTEL EALKSTKDSL
351 ERQRSELEDR HQADIASYQE AIQQLDAELR NTKWEMAAQL REYQDLLNVK

09/847586

401 MLDIEIAAY RKLLEGEECR IGFGPIPFSL PEGLPKIPSV STHIKVKSEE
451 KIKVVEKSEK ETVIVEEQTE ETQVTEEVTE EEEKEAKEEE GKEEEGGEETK SPPAEEAASP EKEAKSPVKE EAKSPAEEAKS PEKEEAKSPA
501 EAEGGEEETK SPPAEEAASP EKEAKSPVKE EAKSPAEEAKS PEKEEAKSPA
551 EVKSPEAKS PAKEEAKSPP EAKSPEKEA KSPAEVKSPE KAKSPAEEA
601 KSPAEAKSPE KAKSPVKEEA KSPAEAKSPV KEEAKSPAEV KSPEAKSPT
651 KEEAKSPEKA KSPEAKSPE KEEAKSPEKA KSPVKAEEAKS PEAKSPVKA
701 EAKSPEAKS PVKEEAKSPE KAKSPVKEEA KSPAEAKSPE KEEAKTPEKA
===== =
751 KSPVKEEAKS PEAKSPEKA KTLDVKSPEA KTPAKEEARS PADKFPEAK
===== =
801 SPVKEEVKSP EKAKSPLKED AKAPEKEIPK KEEVKSPVKE EEPQEVVK
851 EPPKKAEEEK APATPKTEEK KDSKKEEAPK KEAPKPKVVE KKEPAVEPK
901 ESKVEAKKEE AEDKKKVPTP EKEAPAKVEV KEDAKPKETK EVAKKEPDDA
951 KAKEPSKPAE KKEAAPEKKD TKEEKAKKPE EKPTEAKAK EDDKTLKEP
1001 SKPKAEKAEC SSSTDQKDSK PPEKATEDKA AKGK

HITS AT: 708-739, 750-767

REFERENCE 1: 130:292252

L4 ANSWER 26 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 147388-28-1 REGISTRY
CN Phosphoprotein NF-H (rabbit isoform 1 C-terminal fragment) (9CI)
(CA INDEX NAME)
CI MAN
SQL 606

SEQ 1 EKETVIVEEQ TEEIQVTEEV TEEEKEAKE EGGEEEEAK SPTEGGAASP
51 EEEAKSPAEEA KSPVKEEAKS PAEAKSPAEEA KSPAEAKSPE KAKSPVKEEA
===== =
101 KSPEAKSPV KEEAKSPAEEA KSPEAKSPA EAKSPEAKS PVKEEAKSPE
===== =
151 KAKSPAEEAKS PEAKSPAEEA KSPEAKSPV KEEAKSPEKA KSPVKEEAKS
===== =
201 PAEAKSPEKA KSPVKEEAKS PEAKSPAEEA KSPVKEEAKS PEAKSPEKE
===== =
251 EAKSPAEEAKS PEAKSPEKA KSPVEVKSPA EAKSPEAKS PVKEEAKSPE
===== =
301 KAKSPVKEEA KSPEAKSPV KEEAKSPEKA KSPVKEEAKS PEAKSPVKE
===== =
351 EAKSPEAKS PVKEEAKSPE KAKSPEAKS PVKEEAKSPE KAKSPVKEEA
===== =
401 KSPEAKSPV KEEAKSPEKE TPKKEEVVK EPPKKVEETA PAPPKVEKDS
===== =
451 KKDEAPKKEA PKPAVEKPKE STAEAKKDEA EDKKKAAPAK MEGKEEAKPK
501 EKTEVAKKEP EDAKAKEPSK PTEKEPEKPK KEETPAAPVK KEAKEEARKP
551 EEPKTEAKA KEDDKALSKE PSKPKTEKAE KSSSTDQKDS RPPEKATEDK
601 AAKGEK

HITS AT: 92-109, 138-155, 176-193, 210-227, 230-247, 288-375,
378-409

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 118:206731

L4 ANSWER 27 OF 27 REGISTRY COPYRIGHT 2004 ACS on STN
RN 119213-37-5 REGISTRY

Searcher : Shears 571-272-2528

09/847586

CN Phosphoprotein NF-H (human clone HW10/HW12 subunit protein moiety reduced) (9CI) (CA INDEX NAME)
CI MAN
SQL 1054

SEQ 1 MMSFGGADAL LGAPFAPLHG GGSLHYALAR KGGAGGTRSA AGSSSGFHSW
51 TRTSVSSVSA SPSRFRGAGA ASSTDSDLTL SNGPEGCMVA VATSRSEKEQ
101 LQALNDRFLAG YIDKVRQLEA HNRSLEGEAA ALRQQQAGRS AMGELYEREV
151 REMRGAVLRL GAARGQLRLE QEHLLEDIAH VRQRLDDEAR QREEAEAAAR
201 ALARFAQEAE AARVDSLQKKA QALQEECGYL RRHHQEEVGE LLGQIQGSGA
251 AQAQMQAETR DALKCDVTSA LREIRAQLEG HAVQSTLQSE EWFRVRLDRL
301 SEA AKVNTDA MRS AQEEITE YRRQLQARTT ELEALKSTKD SLERQRSELE
351 DRHQADIASY QEAIQQLDAE LRNTKWE MA QLREYQDLLN VKM ALDIEIA
401 AYRK LLEGE CRIGFGPIFF SLPEGLPKIP SVSTHIKVKS EEKIKVVEKS
451 EKETVIVEEQ TEETQVTEEV TEEEKEAKE EEGKEEEGGE EEEAEGGEEE
501 TKSPPAEEAA SPEKEAKSPV KEEAKSPA EA KSPEKEAKS PAEVKSPEKA
551 KSPAKEEAKS PPEAKSPEKE EAKSPA EVKSPEAKS PEKA KSPEAKSPE
601 PEKEEAKSPA EVKSPEAKS PAKEEAKSPA EAKSPEAKS PVKEEAKSPA
651 EAKSPVKEEA KSPAEVKSPE KAKSPTKEEA KSPAKSPE KEEAKSPEKA
701 KSPVKA EAKS PEAKSPVKA EAKSPEAKS PVKEEAKSPE KAKSPVKEEA
===== =====
751 KSPEAKSPV KEEAKTPEKA KSPVKEEAKS PEAKSPEKA KTLDVKSPEA
===== =====
801 KTPAKKEEARS PADKFPEKAK SPVKEEVKSP EKAKSPLKAD AKAPEKEIPK
851 KEEVKSPVKE EEKPKQEVVKV EPPKKAEEEK APATPKTEEK KDSKKEEAPK
901 KEAPKPKVEE KKEPAVEKPK ESKVEAKKEE AEDKKKVPTP EKEAPAKVEV
951 KEDAKPKKEKT EVAKKEPDDA KAKEPSKPAE KKEAAPEKKD TKEEKAKKPE
1001 EKP KTEAKAK EDDKTL SKEP SKPKA EAKK SSSTDQKDSK PPEKATEDKA
1051 AKGK

HITS AT: 728-759, 770-787

REFERENCE 1: 110:89623

=> fil hom
FILE 'HOME' ENTERED AT 11:49:53 ON 26 MAY 2004